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<150> US 08/869,852

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<150> US 08/829,536

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<150> US 08/815,255

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<150> US 08/799,861

<151> 1997-02-13

<160> 6

<170> PatentIn version 3.1

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<212> DNA

<213> Homo sapiens

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agg cac ggc cca gga ccc agg gag gcg cgg gga gcc agg cct ggg ccc 96  
Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro  
20 25 30

cgg gtc ccc aag acc ctt gtg ctc gtt gtc gcc gcg gtc ctg ctg ttg 144  
Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu  
35 40 45

gtc tca gct gag tct gct ctg atc acc caa caa gac cta gct ccc cag 192  
Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln  
50 55 60

cag aga gcg gcc cca caa caa aag agg tcc agc ccc tca gag gga ttg 240  
 Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu  
 65 70 75 80

tgt cca cct gga cac cat atc tca gaa gac ggt aga gat tgc atc tcc 288  
 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser  
 85 90 95

tgc aaa tat gga cag gac tat agc act cac tgg aat gac ctc ctt ttc 336  
 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe  
 100 105 110

tgc ttg cgc tgc acc agg tgt gat tca ggt gaa gtg gag cta agt ccg 384  
 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro  
 115 120 125

tgc acc acg acc aga aac aca gtg tgt cag tgc gaa gaa ggc acc ttc 432  
 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe  
 130 135 140

cgg gaa gaa gat tct cct gag atg tgc cgg aag tgc cgc aca ggg tgt 480  
 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys  
 145 150 155 160

ccc aga ggg atg gtc aag gtc ggt gat tgt aca ccc tgg agt gac atc 528  
 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile  
 165 170 175

gaa tgt gtc cac aaa gaa tca ggt aca aag cac agt ggg gaa gcc cca 576  
 Glu Cys Val His Lys Glu Ser Gly Thr Lys His Ser Gly Glu Ala Pro  
 180 185 190

gct gtg gag gag acg gtg acc tcc agc cca ggg act cct gcc tct ccc 624  
 Ala Val Glu Glu Thr Val Thr Ser Ser Pro Gly Thr Pro Ala Ser Pro  
 195 200 205

tgt tct ctc tca ggc atc atc ata gga gtc aca gtt gca gcc gta gtc 672  
 Cys Ser Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val  
 210 215 220

ttg att gtg gct gtg ttt gtt tgc aag tct tta ctg tgg aag aaa gtc 720  
 Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys Val  
 225 230 235 240

ctt cct tac ctg aaa ggc atc tgc tca ggt ggt ggt ggg gac cct gag 768  
 Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp Pro Glu  
 245 250 255

cgt gtg gac aga agc tca caa cga cct ggg gct gag gac aat gtc ctc 816  
 Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp Asn Val Leu  
 260 265 270

aat gag atc gtg agt atc ttg cag ccc acc cag gtc cct gag cag gaa 864  
 Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro Glu Gln Glu  
 275 280 285

atg gaa gtc cag gag cca gca gag cca aca ggt gtc aac atg ttg tcc 912  
 Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser  
 290 295 300

ccc ggg gag tca gag cat ctg ctg gaa ccg gca gaa gct gaa agg tct 960  
 Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala Glu Arg Ser  
 305 310 315 320

cag agg agg agg ctg ctg gtt cca gca aat gaa ggt gat ccc act gag 1008  
 Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp Pro Thr Glu  
 325 330 335

act ctg aga cag tgc ttc gat gac ttt gca gac ttg gtg ccc ttt gac 1056  
 Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe Asp  
 340 345 350

tcc tgg gag ccg ctc atg agg aag ttg ggc ctc atg gac aat gag ata 1104  
 Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile  
 355 360 365

aag gtg gct aaa gct gag gca gcg ggc cac agg gac acc ttg tac acg 1152  
 Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr  
 370 375 380

atg ctg ata aag tgg gtc aac aaa acc ggg cga gat gcc tct gtc cac 1200  
 Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His  
 385 390 395 400

acc ctg ctg gat gcc ttg gag acg ctg gga gag aga ctt gcc aag cag 1248  
 Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln  
 405 410 415

aag att gag gac cac ttg ttg agc tct gga aag ttc atg tat cta gaa 1296  
 Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu  
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ggt aat gca gac tct gcc atg tcc taa 1323  
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Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro  
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Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu  
 35 40 45

Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln  
 50 55 60

Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu  
65 70 75 80

Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser  
85 90 95

Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe  
100 105 110

Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro  
115 120 125

Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe  
130 135 140

Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys  
145 150 155 160

Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile  
165 170 175

Glu Cys Val His Lys Glu Ser Gly Thr Lys His Ser Gly Glu Ala Pro  
180 185 190

Ala Val Glu Glu Thr Val Thr Ser Ser Pro Gly Thr Pro Ala Ser Pro  
195 200 205

Cys Ser Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val  
210 215 220

Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys Val  
225 230 235 240

Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp Pro Glu  
245 250 255

Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp Asn Val Leu  
260 265 270

Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro Glu Gln Glu  
275 280 285

Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser  
290 295 300

Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala Glu Arg Ser  
305 310 315 320

Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp Pro Thr Glu  
325 330 335

Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe Asp  
340 345 350

Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile  
355 360 365

Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr  
370 375 380

Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His  
385 390 395 400

Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln  
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Gly Asn Ala Asp Ser Ala Met Ser  
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<223> "n" = a, t, g, or c

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ttt gac tcc tgg gag ccg ctc atg agg aag ttg ggc ctc atg gac aat 95  
 Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn  
 20 25 30

gag ata aag gtg gct aaa gct gag gca gcg ggc cac agg gac acc ttg 143  
 Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu  
 35 40 45

tnc acn atg ctg at 157  
 Xaa Xaa Met Leu  
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Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu  
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Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Xaa  
 35 40 45

Xaa Met Leu  
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 cagccgcacg cggcgcacat cgggcagcgt tgggtcctgg ccacgggtgc gcatgatcgt 240  
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D1  
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ataaaaaatag gcgtatcacg aggcccttct gtcttcaag 3159

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